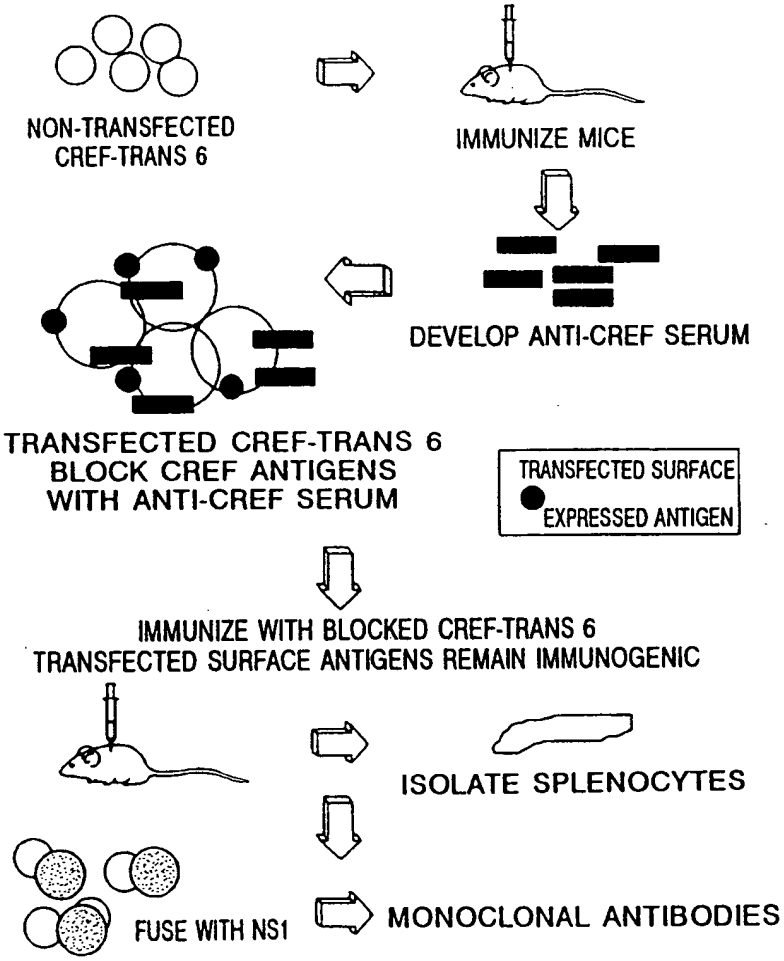

FIG. 1

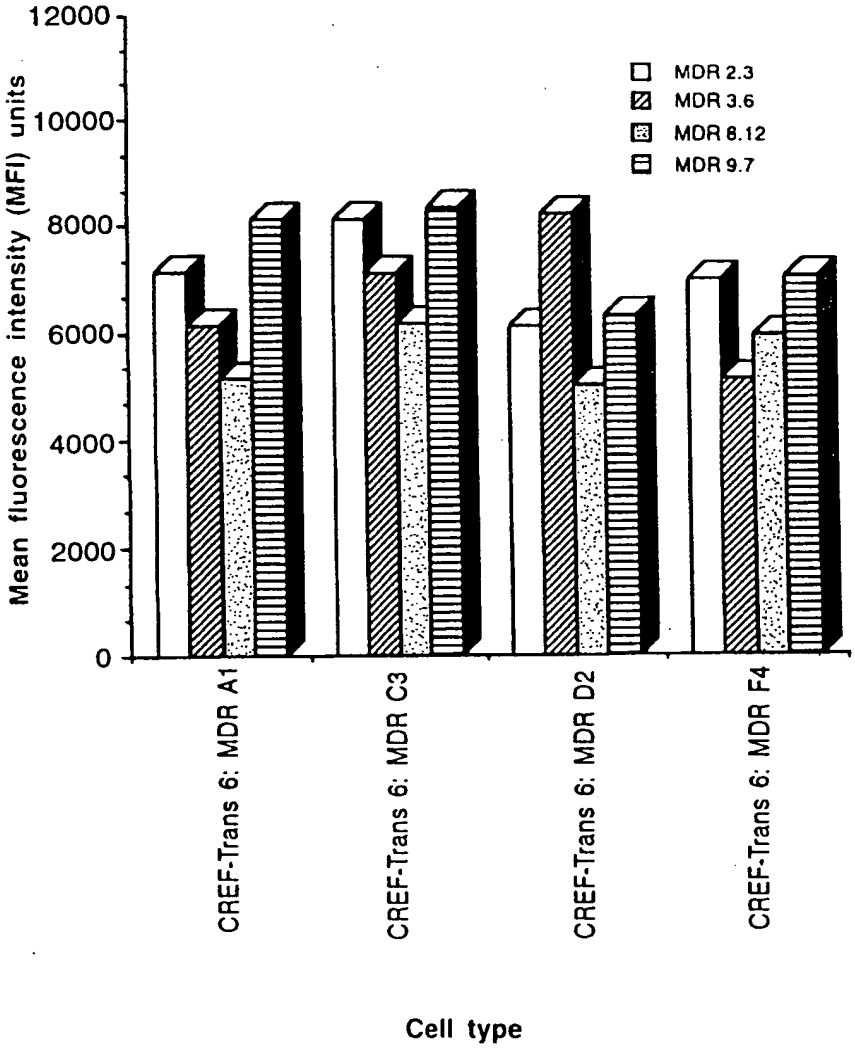
12000
10000
8000
6000
4000
2000
0
Mean fluorescence intensity (MFI) units
MDR 2.3
MDR 3.6
MDR 8.12
MDR 9.7
CREF-Trans 6: MDR A1
CREF-Trans 6: MDR C3
CREF-Trans 6: MDR D2
CREF-Trans 6: MDR F4
Cell type

FIG.2

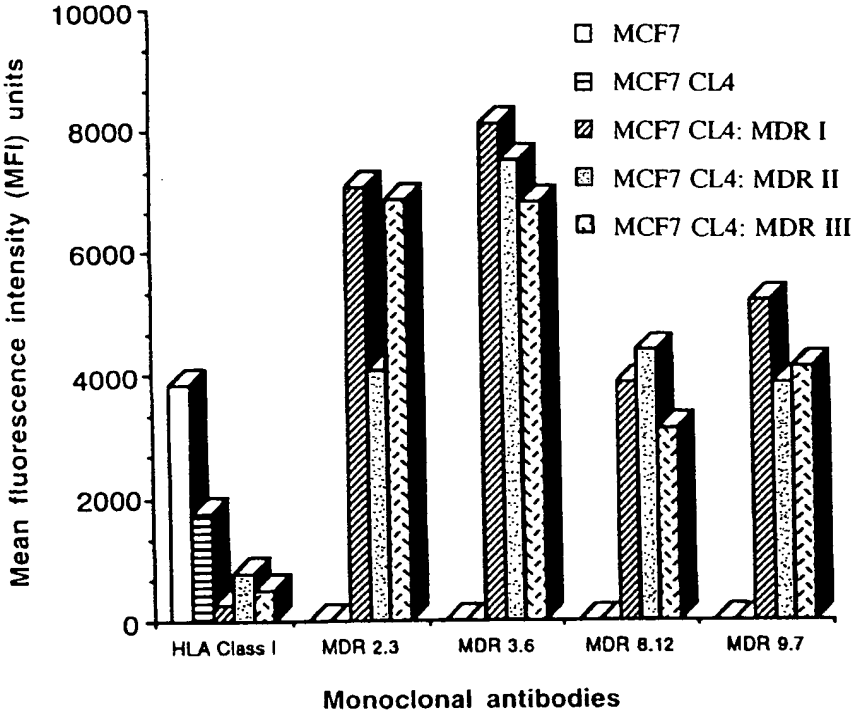
10000
8000
6000
4000
2000
0
Mean fluorescence intensity (MFI) units
MCF7
MCF7 CL4
MCF7 CL4: MDR I
MCF7 CL4: MDR II
MCF7 CL4: MDR III
HLA Class I
MDR 2.3
MDR 3.6
MDR 8.12
MDR 9.7
Monoclonal antibodies

FIG.3

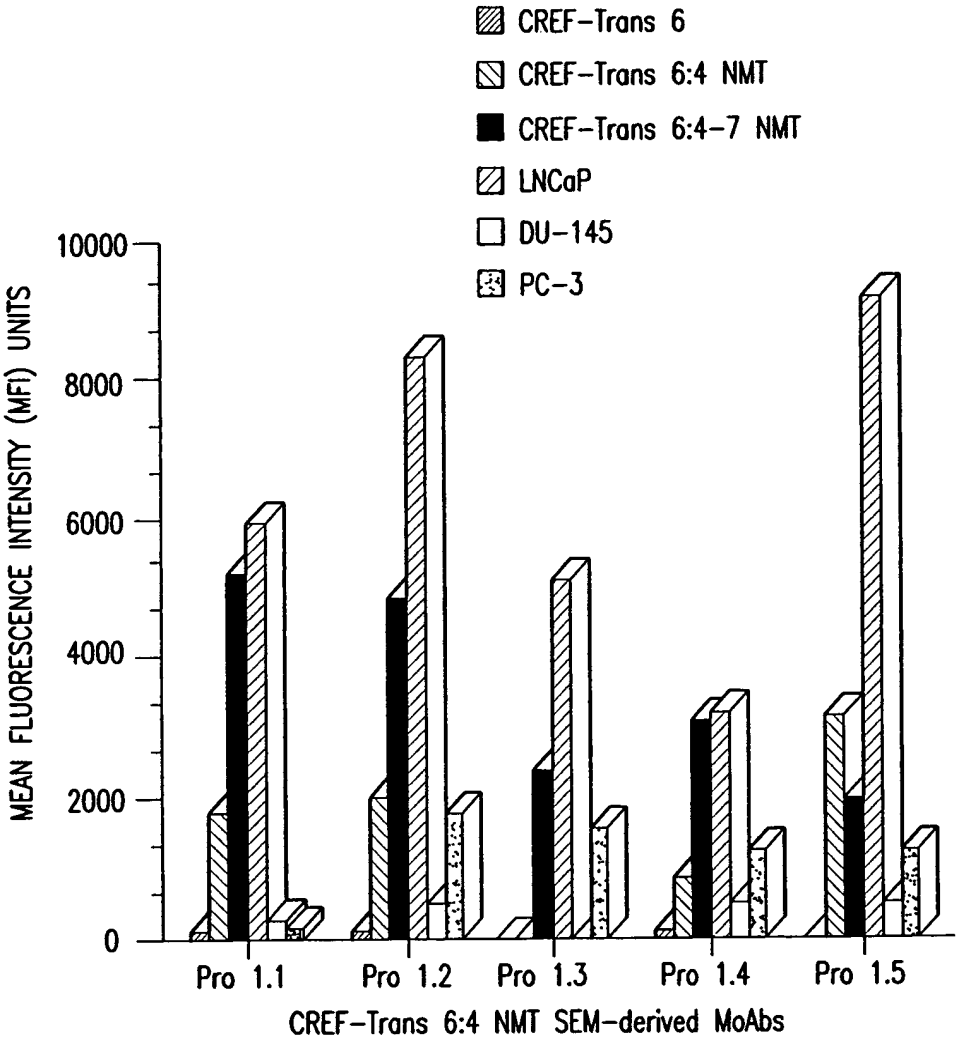
CREF-Trans 6
CREF-Trans 6:4 NMT
CREF-Trans 6:4-7 NMT
LNCaP
DU-145
PC-3
MEAN FLUORESCENCE INTENSITY (MFI) UNITS
10000
8000
6000
4000
2000
0
Pro 1.1
Pro 1.2
Pro 1.3
Pro 1.4
Pro 1.5
CREF-Trans 6:4 NMT SEM-derived MoAbs

FIG.4

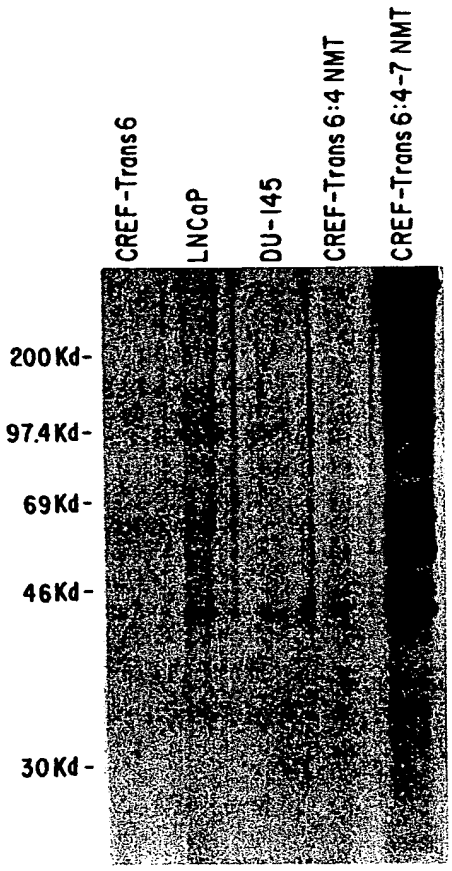

FIG.5

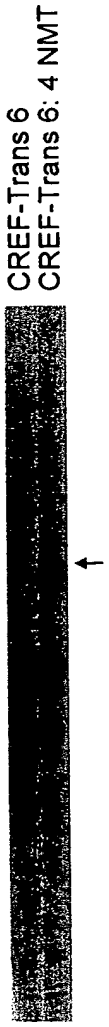

FIG.6

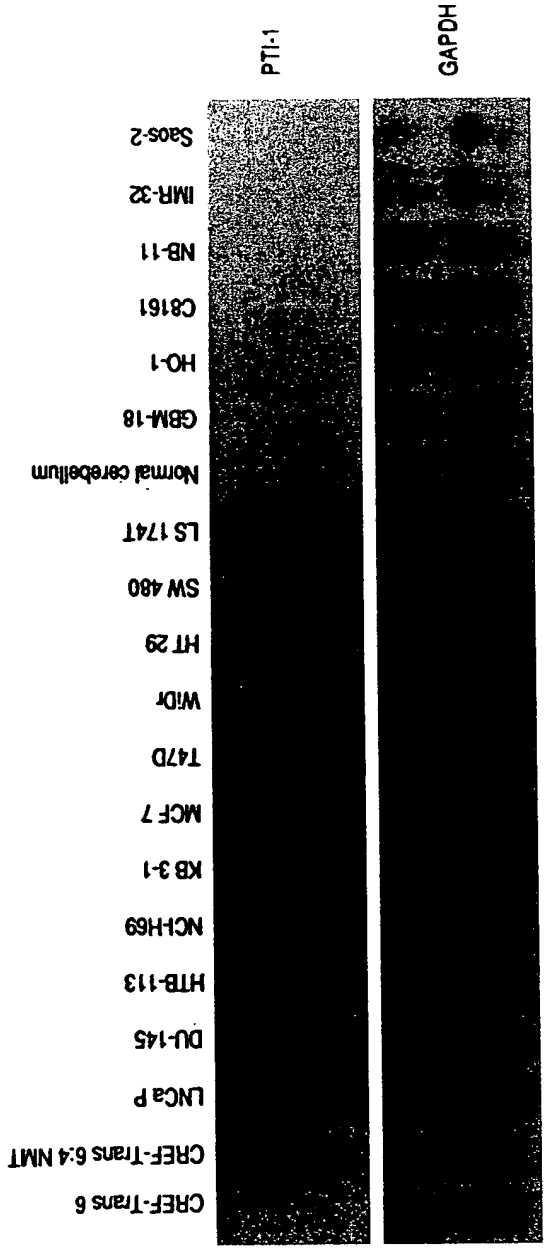

FIG.7

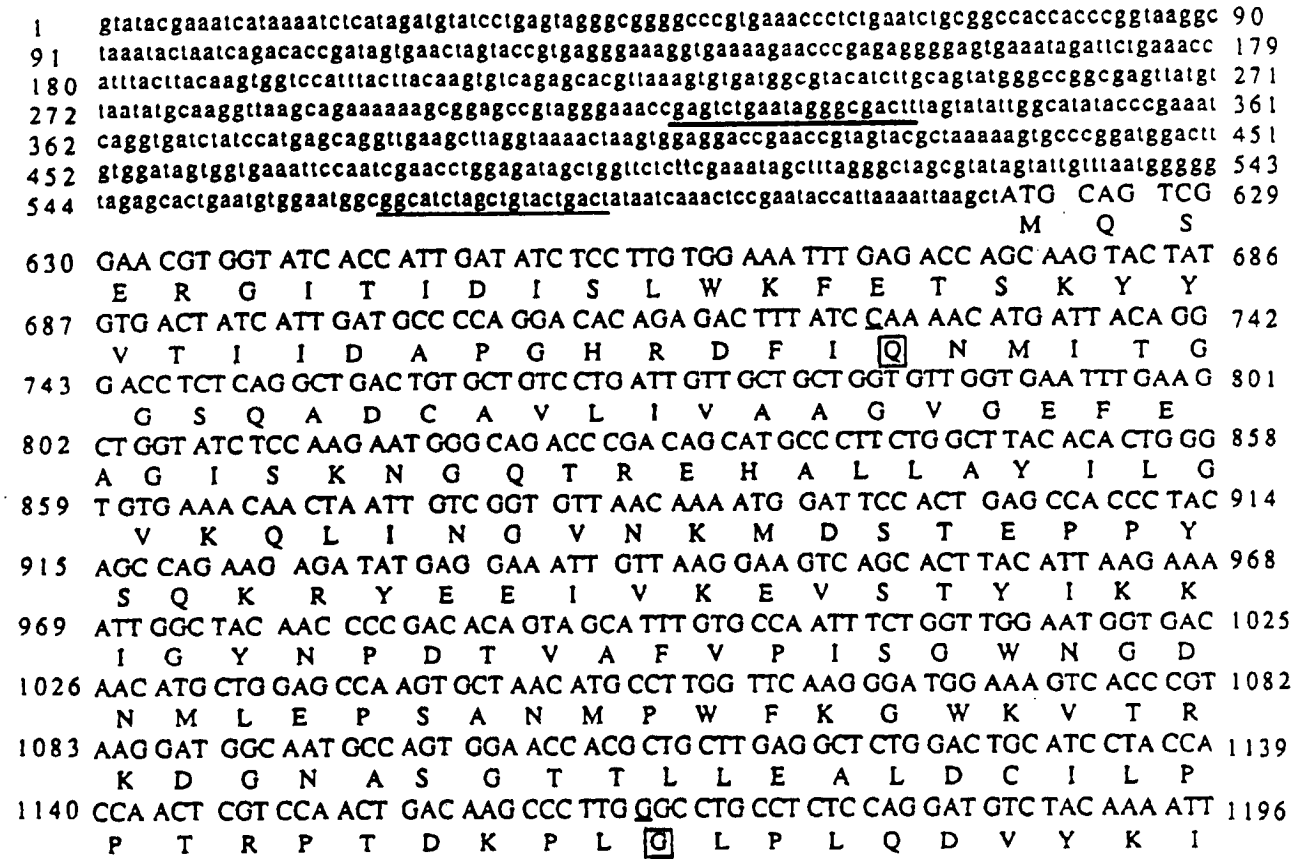
1 gtatacgaaatcataaaatctcatagatgtatcctgagtagggcggggcccgtgaaaccctctgaatctgcggccaccacccggtaaggc 90
91 taaatactaatcagacaccgatagtgaactagtaccgtgagggaaaggtgaaaagaacccgagaggggagtgaaatagattctgaaacc 179
180 atttacttacaagtggtccatttacttacaagtgtcagagcacgttaaagtgtgatggcgtacatcttgcagtatgggccggcgagttatgt 271
272 taatatgcaaggttaagcagaaaaaagcggagccgtagggaaaccgagtctgaatagggcgactttagtatattggcatatacccgaaat 361
362 caggtgatctatccatgagcaggttgaagcttaggtaaaactaagtggaggaccgaaccgtagtacgctaaaaagtgcccggatggactt 451
452 gtggatagtggtgaaattccaatcgaacctggagatagctggttctcttcgaaatagctttagggctagcgtatagtattgtttaatggggg 543
544 tagagcactgaatgtggaatggcggcatctagctgtactgactataatcaaactccgaataccattaaaattaagctATG CAG TCG 629
M Q S
630 GAA CGT GGT ATC ACC ATT GAT ATC TCC TTG TGG AAA TTT GAG ACC AGC AAG TAC TAT 686
E R G I T I D I S L W K F E T S K Y Y
687 GTG ACT ATC ATT GAT GCC CCA GGA CAC AGA GAC TTT ATC CAA AAC ATG ATT ACA GG 742
V T I I D A P G H R D F I Q N M I T G
743 G ACC TCT CAG GCT GAC TGT GCT GTC CTG ATT GTT GCT GCT GGT GTT GGT GAA TTT GAA G 801
G S Q A D C A V L I V A A G V G E F E
802 CT GGT ATC TCC AAG AAT GGG CAG ACC CGA CAG CAT GCC CTT CTG GCT TAC ACA CTG GG 858
A G I S K N G Q T R E H A L L A Y I L G
859 T GTG AAA CAA CTA ATT GTC GGT GTT AAC AAA ATG GAT TCC ACT GAG CCA CCC TAC 914
V K Q L I N G V N K M D S T E P P Y
915 AGC CAG AAG AGA TAT GAG GAA ATT GTT AAG GAA GTC AGC ACT TAC ATT AAG AAA 968
S Q K R Y E E I V K E V S T Y I K K
969 ATT GGC TAC AAC CCC GAC ACA GTA GCA TTT GTG CCA ATT TCT GGT TGG AAT GGT GAC 1025
I G Y N P D T V A F V P I S G W N G D
1026 AAC ATG CTG GAG CCA AGT GCT AAC ATG CCT TGG TTC AAG GGA TGG AAA GTC ACC CGT 1082
N M L E P S A N M P W F K G W K V T R
1083 AAG GAT GGC AAT GCC AGT GGA ACC ACG CTG CTT GAG GCT CTG GAC TGC ATC CTA CCA 1139
K D G N A S G T T L L E A L D C I L P
1140 CCA ACT CGT CCA ACT GAC AAG CCC TTG GGC CTG CCT CTC CAG GAT GTC TAC AAA ATT 1196
P T R P T D K P L G L P L Q D V Y K I

FIG.8A

```
1197 GGT GGT ATT GGT ACT GTT CCT GTT GGC CGA GTG GAG ACT GGT GTT CTC AAA CCC GGT 1253
       G   G   I   G   T   V   P   V   G   R   V   E   T   G   V   L   K   P   G
1254 ATG GTG GTC ACC TTT CGT CCA GTC AAC GTT ACA ACG GAA GTA AAA TCT GTC GAA ATG 1310
       M   V   V   T   F  [G]  P   V   N   V   T   T   E   V   K   S   V   E   M
1311 CAC CAT GAA GCT TTG GGT GAA GCT CTT CCT GGG GAC AAT GTG GGC TTC AAT GTC AAG 1367
       H   H   E   A   L  [G]  E   A   L   P   G   D   N   V   G   F   N   V   K
1368 AAT GTG TCT GTC AAG GAT GTT CGT CGT GGC AAC GTT GCT GGT GAC AGC AAA AAT GAC 1424
       N   V   S   V   K   D   V   R   R   G   N   V   A   G   D   S   K   N   D
1425 CCA CCA ATG GAA GCA GCT GGC TTC CCT GCT CAG GTG ATT ATC CTG AAC CAT CCA GGC 1481
       P   P   M   E   A   A   G   F  [P]  A   Q   V   I   I   L   N   H   P   G
1482 CAA ATA AGC GCC GGC TAT GCC CCT GTA TTG GAT TGC CAC ACG GCT CAC ATT GCA TGC 1538
       Q   I   S   A   G   Y   A   P   V   L   D   C   H   T   A   H   I   A   C
1539 AAG TTT GCT GAG CTG AAG GAA AAG ATT GAT CGC CGT TCT GGT AAA AAG CTG GAA 1592
       K   F   A   E   L   K   E   K   I   D   R   R   S   G   K   K   L   E
1593 GAT GGC CCT AAA TTC TTG AAG TCT GGT GAT GCT GCC ATT GTT GAT ATG GTT CCT GGC 1649
       D   G   P   K   F   L   K   S   G   D   A   A   I   V   D   M   V   P   G
1650 AAG CCC ATG TGT GTT GAG AGC TTC TCA GAC TAT CCA CCT TTG GGC TGC TTT GCT GTT 1706
       K   P   M   C   V   E   S   F   S   D   Y   P   P   L   G  [C]  F   A   V
1707 CGT GAT ATG AGA CAG ACA GTT GCG GTG GGT GTC ATC AAA GCA GTG GAC AAG AAG GCT 1763
       R   D   M   R   Q   T   V   A   V   G   V   I   K   A   V   D   K   K   A
1764 GCT GGA GCT GGC AAG GTC ACC AAG TCT GCC CAG AAA GCT CAG AAG GCT AAA TGA 1817
       A   G   A   G   K   V   T   K   S   A   Q   K   A   Q   K   A   K  ter
1818 atattatccctaatacctcccaccccactcttaatcagtggtggaagaccggtctcagaactgtttgtttcaattggccatttaagtttagt 1904
1910 agtaaaagactggttaatgataacaatgcatcgtaaaaccttcagaaggaaaggagaatgttttgtggaccacgttggttttctttttgc 1996
1997 gtgtggcagttttaagttattagttttaaaatcagtacttttaatggaaacaacttgacccccaaatttgtcacagaatttgggacccat 1089
2090 taaaaaggttaactgggaaaaaaaaaaaaaaaa                                                          2123
```

FIG.8B

```
(E)1                                                    MGKEKTHINIVVIGH  15

(E)16   VDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAAEMGKGSFKYAWVLDKLKAER  67
(P)1                                                        MQS   3

(E)68   ERGITIDISLWKFETSKYYVTIIDAPGHRDFIKNMITGTSQADCAVLIVAAGV 120
(P)4    ERGITIDISLWKFETSKYYVTIIDAPGHRDFIQNMITGTSQADCAVLIVAAGV  56

(E)121  GEFEAGISKNGQTREHALLAYTLGVKQLIVGVNKMDSTEPPYSQKRYEEIVKE 173
(P)57   GEFEAGISKNGQTREHALLAYTLGVKQLIVGVNKMDSTEPPYSQKRYEEIVKE 109

(E)174  VSTYIKKIGYNPDTVAFVPISGWNGDNMLEPSANMPWFKGWKVTRKDGNA 223
(P)110  VSTYIKKIGYNPDTVAFVPISGWNGDNMLEPSANMPWFKGWKVTRKDGNA 159

(E)224  SGTTLLEALDCILPPTRPTDKPLRLPLQDVYKIGGIGTVPVGRVETGVLKPGM 276
(P)160  SGTTLLEALDCILPPTRPTDKPLGLPLQDVYKIGGIGTVPVGRVETGVLKPGM 212

(E)277  VVTFAPVNVTTEVKSVEMHHEALSEALPGDNVGFNVKNVSVKDVRRGNV  325
(P)213  VVTFGPVNVTTEVKSVEMHHEALGEALPGDNVGFNVKNVSVKDVRRGNV  261

(E)326  AGDSKNDPPMEAAGFTAQVIILNHPGQISAGYAPVLDCHTAHIACKFAELK 376
(P)262  AGDSKNDPPMEAAGFPAQVIILNHPGQISAGYAPVLDCHTAHIACKFAELK 312

(E)377  EKIDRRSGKKLEDGPKFLKSGDAAIVDMVPGKPMCVESFSDYPPLGRFAVRD 428
(P)313  EKIDRRSGKKLEDGPKFLKSGDAAIVDMVPGKPMCVESFSDYPPLGCFAVRD 364

(E)429  MRQTVAVGVIKAVDKKAAGAGKVTKSAQKAQKAK                   462
(P)365  MRQTVAVGVIKAVDKKAAGAGKVTKSAQKAQKAK                   398
```

FIG.8C

Human EF-1α	Amino Acid	K (100)	R (247)	A (281)	S (300)	T (341)	R (423)
	Codon	AAA	CGC	GCT	AGT	ACT	CGC
	Nucleotide	A	C	C	A	A	C

PTI-1	Amino Acid	Q (36)	G (183)	G (217)	G (236)	P (277)	C (359)
	Codon	CAA	GGC	GGT	GGT	CCT	TGC
	Nucleotide	C	G	G	G	C	T

FIG.8D

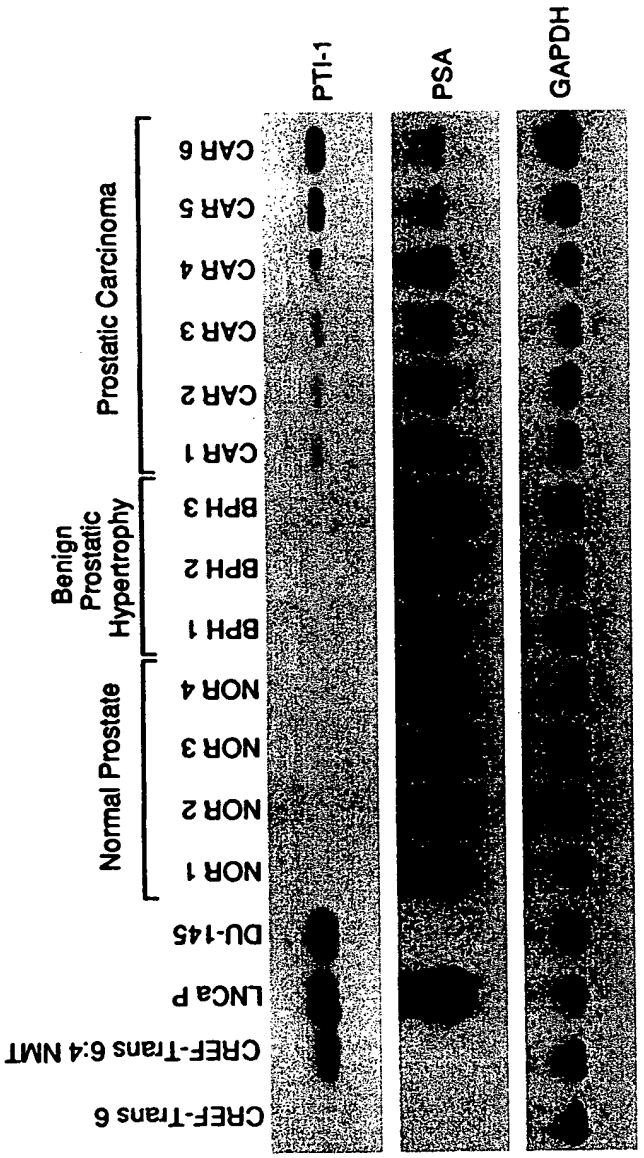

FIG.9

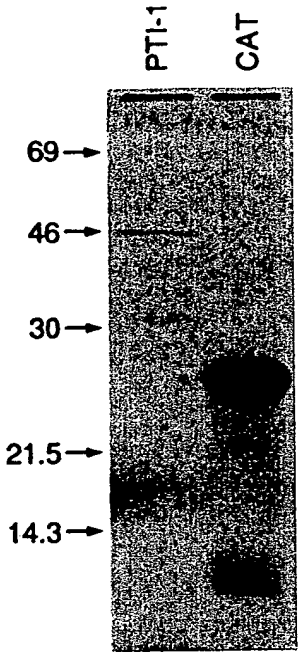

FIG.10

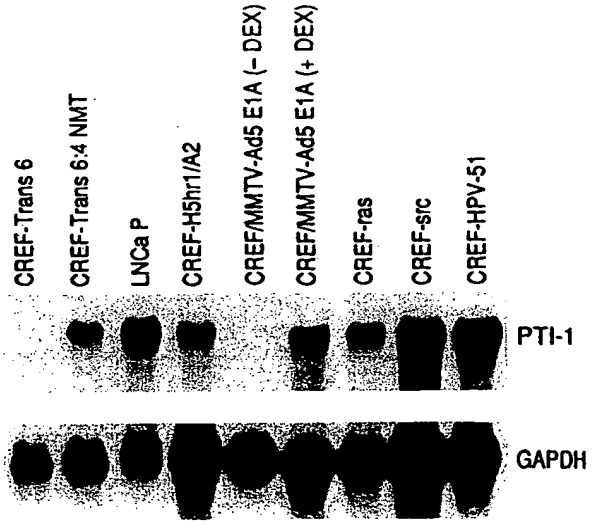

FIG.11

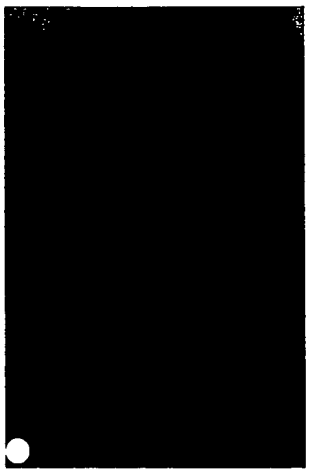

FIG.12B

FIG.12D

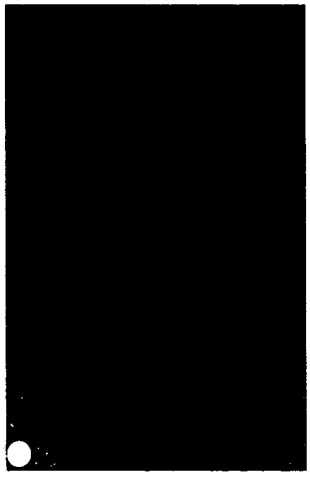

FIG.12A

FIG.12C

1 CGGACCGAGC TCCGTTGCAT TTTGATGAAT CCATAGTCAA ATTAGCGAGA

51 CACGTTGCGA ATTGAAACAT CTTAGTAGCA ACAGGAAAAG AAAATAAATA

101 ATGATTTCGT CAGTAGTGGC GAGCGAAAGC GAAAGAGCCC AAACCTGTAA

151 AGGGGGGTTG GTAGGACATC TTACATTGAG TTACAAAATT TTATGATAGT

201 AGAAGAAGTT GGGAAAGCTT CAACATAGAA GGTGATATTC CTGTATACGA

251 AATCATAAAA TCTCATAGAT GTATCCTGAG TAGGGCGGGG TACGTGAAAC

301 CCTGTCTGAA TCTGCCCGGG ACCACCCGTA AGGCTAAATA CTAATCAGAC

351 ACCGATAGTG AACTAGTACC GTGAGGGAAA GGTGAAAAGA ACCCGAGAGG

401 GGAGTGAAAT AGATTCTGAA ACCATTTACT TACAAGTAGT CAGAGCACGT

451 TAAAGTGTGA TGGCGTACAT CTTGCAGTAT GGGCCGGCGA GTTATGTTAA

501 TATGCAAGGT TAAGCACGAA AAAAGCGGAG CCGTAGGGAA ACCGAGTCTG

551 AATAGGGCGA CTTTAGTATA TTGGCATATA CCCGAAACCA GGTGATCATC

601 CATGAGCAGG TTGAAGCTTA GGTAAAACTA AGTGGAGGAC CGAACCGTAG

651 TACGCTAAAA AGTGCCCGGA TGACTTGTGG ATAGTGGTGA AATTCCAATC

701 GAACCTGGAG ATAGCTGGTT CTCTTCGAAA TAGCTTTAGG GCTAGCGTAT

751 AGTACTGTTT AATGGGGGTA GAGCACTGAA TGTGGAATGG CGGCATCTAG

801 CTGTACTGAC TATAATCAAA CTCCGAATAC CATTAAAATT AAGCTATGCA

851 GTCGGAACGT GGGTGATAAC GTCCACGCTC GCGAGGGAAA CAACCCAGAT

901 CCGTCAGCTA AGGTCCCAAA ATTGTGTTAA GTGAGAAAGG TTGTGGAGAT

951 TTCATAAACA ACTAGGAAGT TGGTTTAGAA GCAGCCACCT TTTAAAGAGT

1001 GCGTAATTGC TCACTAGTCA AGAGATCTTG CGCCAATAAT GTAACGGGAC

1051 TCAAACACAA TACCCAAGCT ACGGGCACAT TATGTGCGTT AGGAGAGCGT

1101 TTTAATTTCG TTGAAGTCAG ACCGTGAGAC TGGTGGAGAG ATTAAAAGTT

1151 CGAGAATGCC GGCATGAGTA ACGATTCGAA GTGAGAATCT TCGACGCCTA

1201 TTGGGAAAGG TTTCCTGGGC AAGGTTCTCC ACCCAGGGTT AGTCAGGGCC

1251 TAAGATGAGG CAGAAATGCA TAGTCGATGG ACAACAGGTT AATATTCCTG

FIG.13A

1301 TACTTGGTAA AAGAATGATG GAGTGACGAA AAAGGATAGT TCTACCACTT

1351 CCACTATGTC CTATCAATAG GAGCTGTATT TGGCATCATA GGAGGCTTCA

1401 TTCACTGATT TCCCCTATTC TCAGGCTACA CCCTAGACCA AACCTACGCC

1451 AAAATCCATT TCACTATCAT ATTCATCGGC GTAAATCTAA CTTTCTTCCC

1501 ACAACACTTT CTCGGCCTAT CCGGAATGAC CCGACCCGAC GTTACTCGGA

1551 CTACCCCGAT GCATACACCA CATGAAACAT CCTATCATCT GTAGGCTCAT

1601 TCATTTCTCT AACAGCAGTA ATATTAATAA TTTTCATGAT TTGAGAAGCC

1651 TTCGCCTTCG AAGCGAAAAG TCCTAATAGT AGAAGAACCC TCCATAAACC

1701 TGGAGTGACT ATATGGATGC CCCCACCCTA CCTCACATTC GAAGAACCCG

1751 TATACATAAA ATCTAGACAA AAAAGGAAGG AAGTGAACGC CCCACAAAAA

1801 AAAAAAAAAA AAAAAAAAA

FIG.13B

1 AACTAAGTGG AGGACCGAAC CGTAGTACGC TAAAAAGTGC CCGGATGACT

51 TGTGGATAGT GGTGAAATTC CAATCGAACC TGGAGATAGC TGGTTCTCTT

101 CGAAATAGCT TTAGGGCTAG CGTATAGTAT TGTTTAATGG GGGTAGAGCA

151 CTGAATGTGG AATCGGCGGC ATCTAGCTGT ACTGACTATA ATCAAACTCC

201 GAATACCATT AAAATTAAGC TATGCAGTCG GAACGTGGGT GATAACCTCC

251 ACTCTCGCGA GGGAAACAAC CCAGATCGTC AGCTAAGGTC CCAAAATTGT

301 GTTAAGTGAG AAAGGTTGTG AGATTTCATA AACAACTAGG AAGTTGGCTT

351 AGAAGCAGCC ACCTTTTAAA GAGTGCGTAA TTGCTCACTA GTCAAGAGAT

401 CTTGCGCCAA TAATGTAACG GGACTCAAAC ACAATACCGA AGCTACGGGC

451 ACATTATGTC GGTTAGGAGA GCGTTTTAAT TTCGTTGAAG TCAGACCGTG

501 AGACTGGTGG AGAGATTAAA AGTTCGAGAA TGCCCGGCAT GAGTAACGAT

551 TCGAAGTGAG AATCTTCGAC GCCTATTGGG AAAGGTTTCC TGGGCAAGGT

601 TCGTCCACCC AGGGTTAGTC AGGGCCTAAG ATGAGGCAGA AATGCATAGT

651 CGATGGACAA CAGGTTAATA TTCCTGTACT TGGTAAAAGA ATGATGGAGT

701 GACGAAAAAG GATAGTTCTA CCACTTACTG GATTGTGGGG TAAGCAACAA

751 GAGAGTTATA TAGGCAAATC CGTATAGCAT AATCTTGAGT TGTGATGCAT

801 AGTGAAGACT TCGGTCGAGT AACGAATTGA ATCGATTTCA TGTTTCCAAG

851 AAAAGCTTCT AGTGTTAATT TTTTATCAAC CTGTACCGAG AACGAACACA

901 CGTTCCCAAG ATGAGTATTC TAAGGCGAGC GAGAAAACCA ATGTTAAGGA

951 ACTCTGCAAA ATAACCCCGT AAGTTCGCGA GAAGGGGCGC CTATTTTTAA

1001 TAGGCCACAG AAAATAGGGG GGCAACTGTT TATCAAAAAC ACAGCTCTCT

1051 GCTAAGTTGT AAAACGACGT ATAGAGGGTG AAGCCTGCCC AGTCCCGAAG

1101 TTAAACGGAG ATGTTAGCTT ACGCAAAGCA TTAAAGTGAA GCCCGGGTGA

1151 ACGGCGGCCG TAACTATAAC GGTCCTAAGG TAGCGAAATT CCTTGTCAAC

1201 TAATTATTGA CCTGCACGAA AGGCGCAATG ATCTCCCTAC TGTCTCAACA

1251 TTGGACTCGG TGAAATTATG GTACCAGTGA AAACGCAGGT TACCCGCATC

FIG.14A

1301 AAGACGAAAA GACCCCGTGG AGCTTTACTA TAACTTCGTA TTGAAAATTG

1351 GTTTAGCATG TGTAGGATAG GCGGGAGACT TTGAAGCTGG GACGCTAGTT

1401 CTAGTGGAGT CAACCTTGAA ATACCACCCT TGCTAAATTG ATTTTCTAAC

1451 CCGTTCCCCT TATCTGGAAG GAGACAGTGC GTGGTGGGTA GTTTGACTGG

1501 GCGGTCGCCT CCTAAAGTGT AACGGAGGCG TTCAAAGCTA CACTCAATAT

1551 GGTCAGAAAC CATATGCAGA GCACAAAGGT AAAAGTGTGG TTGACTGCAA

1601 GACTTACAAG TCGAGCAGGT GCGAAAGCAG GACTTAGTGA TCCGGCGGTA

1651 CATTGTGGAA TGGCCGTCGC TCAACGGATA AAAGTCACCC CGGGGATAAC

1701 AGGCTAATCT TCCCCAAGAG ATCACATCGA CGGGAAGGTT TGGCACCTCG

1751 ATGTCGGCTC ATCGCATCCT GGAGCTGGAG TCGGTTCCAA GGGTTTGCTG

1801 TTCGCCAATT AAAGCGGTAC GTGAGCTGGG TTCAGAACGT CGTGAGACAG

1851 TTCGGTCCTC CACTTAGTT

FIG.14B

- 1 CGGCACGAGC GGCACGAGAG AAGAGACTCC AATCGACAAG AAGCTGGAAA
- 51 AGAATGATGT TGTCCTTAAA CAACCTACAG AATATCATCT ATAACCCGGT
- 101 AATCCCGTTT GTTGGCACCA TTCCTGATCA GCTGGATCCT GGAACTTTGA
- 151 TTGTGATACG TGGGCATGTT CCTAGTGACG CAGACAGATT CCAGGTGGAT
- 201 CTGCAGAATG GCAGCAGCGT GAAACCTCGA GCCGATGTGG CCTTTCATTT
- 251 CAATCCTCGT TTCAAAAGGG CCGGCTGCAT TGTTTGCAAT ACTTTGATAA
- 301 ATGAAAAATG GGGACGGGAA GAGATCACCT ATGACACGCC TTTCAAAAGA
- 351 GAAAAGTCTT TTGAGATCGT GATTATGGTG CTGAAGGACA AATTCCAGGT
- 401 GGCTGTAAAT GGAAAACATA CTCTGCTCTA TGGCCACAGG ATCGGCCCAG
- 451 AGAAAATAGA CACTCTGGGC ATTTATGGCA AAGTGAATAT TCACTCAATT
- 501 GGTTTTAGCT TCAGCTCGGA CTTACAAAGT ACCCAAGCAT CTAGTCTGGA
- 551 ACTGACAGAG ATAGTTAGAG AAAATGTTCC AAAGTCTGGC ACGCCCCAGC
- 601 TTAGCCTGCC ATTCGCTGCA AGGTTGAACA CCCCCATGGG CCCTGGACGA
- 651 ACTGTCGTCG TTCAAGGAGA AGTGAATGCA AATGCCAAAA GCTTTAATGT
- 701 TGACCTACTA GCAGGAAAAT CAAAGGATAT TGCTCTACAC TTGAACCCAC
- 751 GCCTGAATAT TAAAGCATTT GTAAGAAATT CTTTTCTTCA GGAGTCCTGG
- 801 GGAGAAGAAG AGAGAAATAT TACCTCTTTC CCATTTAGTC CTGGGATGTA

FIG.15A

- 851 CTTTGAGATG ATAATTTATT GTGATGTTAG AGAATTCAAG GTTGCAGTAA
- 901 ATGGCGTACA CAGCCTGGAG TACAAACACA GATTTAAAGA GCTCAGCAGT
- 951 ATTGACACGC TGGAAATTAA TGGAGACATC CACTTACTGG AAGTAAGGAG
- 1001 CTGGTAGCCT ACCTACACAG CTGCTACAAA AACCAAAATA CAGAATGGCT
- 1051 TCTGTGATAC TGGCCTTGCT GAAACGCATC TCACTGGTCA TTCTATTGTT
- 1101 TATATTGTTA AAATGAGCTT GTGCACCATT AGGTCCTGCT GGGTGTTCTC
- 1151 AGTCCTTGCC ATGACGTATG GTGGTGTCTA GCACTGAATG GGGAAACTGG
- 1201 GGGCAGCAAC ACTTATAGCC AGTTAAAGCC ACTCTGCCCT CTCTCCTACT
- 1251 TTGGCTGACT CTTCAAGAAT GCCATTCAAC AAGTATTTAT GGAGTACCTA
- 1301 CTATAATACA GTAGCTAACA TGTATTGAGC ACAGATTTTT TTTGGTAAAT
- 1351 CTGTGAGGAG CTAGGATATA TACTTGGTGA AACAAACCAG TATGTTCCCT
- 1401 GTTCTCTTGA GCTTCGACTC TTCTGTGCGC TACTGCTGCG CACTGCTTTT
- 1451 TCTACAGGCA TTACATCAAC TCCTAAGGGG TCCTCTGGGA TTAGTTATGC
- 1501 AGATATTAAA TCACCCGAAG ACACTAACTT ACAGAAGACA CAACTCCTTC
- 1551 CCCAGTGATC ACTGTCATAA CCAGTGCTCT GCCGTATCCC ATCACTGAGG
- 1601 ACTGATGTTG ACTGACATCA TTTTCTTTAT CGTAATAAAC ATGTGGCTCT
- 1651 ATTAGCTGCA AGCTTTACCA AGTAATTGGC ATGACATCTG AGCACAGAAA
- 1701 TTAAGCCAAA AAACCAAAGC AAAACAAATA CATGGTGCTG AAATTAACTT

FIG.15B

- 1751 GATGCCAAGC CCAAGGCAGC TGATTTCTGT GTATTTGAAC TTACCCGAAA
- 1801 TCAGAGTCTA CACAGACGCC TACAGAAGTT TCAGGAAGAG CCAAGATGCA
- 1851 TTCAATTTGT AAGATATTTA TGGCCAACAA AGTAAGGTCA GGATTAGACT
- 1901 TCAGGCATTC ATAAGGCAGG CACTATCAGA AAGTGTACGC CAACTAAGGG
- 1951 ACCCACAAAG CAGGCAGAGG TAATGCAGAA ATCTGTTTTG TTCCCATGAA
- 2001 ATCACCAATC AAGGCCTCCG TTCTTCTAAA GATTAGTCCA TCATCATTAG
- 2051 CAACTGAGAT CAAAGCACTC TTCCACTTTA CGTGATTAAA ATCAAACCTG
- 2101 TATCAGCAAG TTAAATGGTT CCATTTCTGT GATTTTTCTA TTATTTGAGG
- 2151 GGAGTTGGCA GAAGTTCCAT GTATATGGGA TCTTTACAGG TCAGATCTTG
- 2201 TTACAGGAAA TTTCAAAGGT TTGGGAGTGG GGAGGGAAAA AAGCTCAGTC
- 2251 AGTGAGGATC ATTCCACATT AGACTGGGGC AGAACTCTGC CAGGATTTAG
- 2301 GAATATTTTC AGAACAGATT TTAGATATTA TTTCTATCCA TATATTGAAA
- 2351 AGGAATACCA TTGTCAATCT TATTTTTTTA AAAGTACTCA GTGTAGAAAT
- 2401 CGCTAGCCCT TAATTCTTTT CCAGCTTTTC ATATTAATGT ATGCAGAGTC
- 2451 TCACCAAGCT CAAAGACACT GGTTGGGGGT GGAGGGTGCC ACAGGGAAAG
- 2501 CTGTAGAAGG CAAGAAGACT CGAGAATCCC CCAGAGTTAT CTTTCTCCAT
- 2551 AAAGACCATC AGAGTGCTTA ACTGAGCTGT TGGAGACTGT GAGGCATTTA
- 2601 GGAAAAAAAT AGCCCACTCA CATCATTCCT TGTAAGTCTT AAGTTCATTT

FIG.15C

- 2651 TCATTTTACG TGGAGGAAAA AAATTTAAAA AGCTATTAGT ATTTATTAAT
- 2701 GAATTTTACT GAGACATTTC TTAGAAATAT GCACTTCTAT ACTAGCAAGC
- 2751 TCTGTCTCTA AAATGCAAGT TGGCCTTTTG CTTGCCACAT TTCTGCATTA
- 2801 AACTTCTATA TTAGCTTCAA AGGCTTTTAA TCTCAATGCG AACATTCTAC
- 2851 GGGATGTTCT TAGATGCCTT TAAAAAGGGG GCAAGATCTA ATTTTATTTG
- 2901 AACCCTCACT TTCCAACTTT CACCATGACC CAGTACTAGA GATTAGGGCA
- 2951 CTTCAAAGCA TTGAAAAAAA TCTACTGATA CTTACTTTCT TAGACAAGTA
- 3001 GTTCTTAGTT AACCACCAAT GGAACTGGGT TCATTCTGAA TCCTGGAGGA
- 3051 GCTTCCTCGT GCCACCCAGT GTTTCTGGGC CCTCTGTGTG AGCAGCCAGG
- 3101 TGTGAGCTGT TTTAGAAGCA GCGTGTTGCC TTCATCTCTC CCGTTTCCCA
- 3151 AAAGAACAAA GGATAAAGGT GACAGTCACA CTCCTGGGTT AAAAAAAGCA
- 3201 TTCCAGAACC ACTTCTCTTT ATGGGCACAA CAACAAAGAA GCTAAGTTCG
- 3251 CCTACCCAAA TGAAAGTAGG CTTTACAGTC AAGTACTTCT GTTGATTGCT
- 3301 AAATAACTTC ATTTTCTTGA AATAGAGCAA CTTTGAGTGA AATCTGCAAC
- 3351 ATGGATACCA TGTATGTAAG ATACTGCTGT ACAGAAGAGT TAAGGCTTAC
- 3401 AGTGCAAATG AGGCGTCAGC TTTGGGTGCT AAAATTAACA AGTCTAATAT
- 3451 TATTACCATC AATCAGGAAG AGATAATAAA TGTTTAAACA AACACAGCAG
- 3501 TCTGTATAAA AATACGTGTA TATTTACTCT TTCTGTGCAC GCTCTATAGC

FIG.15D

- 3551 ATAGGCAGGA GAGGCTTATG TGGCAGCACA AGCCAGGTGG GGATTTTGTA
- 3601 AAGAAGTGAT AAAACATTTG TAAGTAATCC AAGTAGGAGA TATTAAGGCA
- 3651 CCAAAAGTAA CATGGCACCC AACACCCAAA AATAAAAATA TGAAATATGA
- 3701 GTGTGAACTC TGAGTAGAGT ATGAAACACC ACAGAAAGTC TTAGAAATAG
- 3751 CTCTGGAGTG GCTCTCCCAG GACAGTTTCC AGTTGGCTGA ATAGTCTTTT
- 3801 GGCACTGATG TTCTACTTCT TCACATTCAT CTAAAAAAAA AAAAAAAAAA

FIG.15E

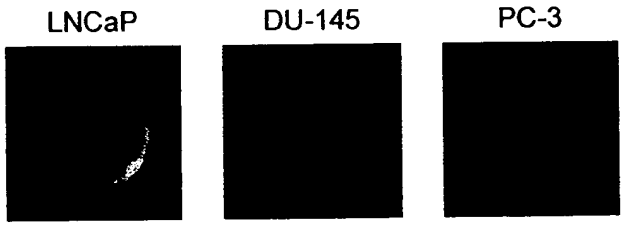

FIG.16A FIG.16B FIG.16C

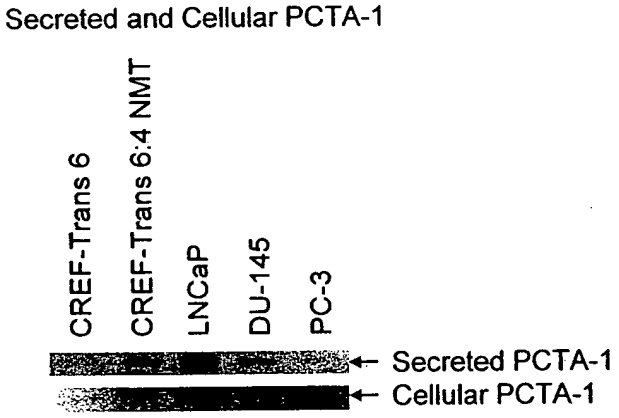

FIG.16D

FIG.17D

FIG.17H

FIG.17C

FIG.17G

FIG.17B

FIG.17F

FIG.17A

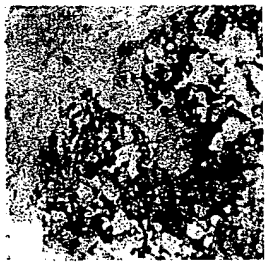

FIG.17E

FIGURE 18A

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  54 ATG ATG TTG TCC TTA AAC AAC CTA CAG AAT ATC ATC TAT AAC CCG GTA ATC CCG TTT GTT
      M   M   L   S   L   N   N   L   Q   N   I   I   Y   N   P   V   I   P   F   V
 114 GGC ACC ATT CCT GAT CAG CTG GAT CCT GGA ACT TTG ATT GTG ATA CGT GGG CAT GTT CCT
      G   T   I   P   D   Q   L   D   P   G   T   L   I   V   I   R   G   H   V   P
 174 AGT GAC GCA GAC AGA TTC CAG GTG GAT CTG CAG AAT GGC AGC AGC GTG AAA CCT CGA GCC
      S   D   A   D   R   F   Q   V   D   L   Q   N   G   S   S   V   K   P   R   A
 234 GAT GTG GCC TTT CAT TTC AAT CCT CGT TTC AAA AGG GCC GGC TGC ATT GTT TGC AAT ACT
      D   V   A   F   H   F   N   P   R   F   K   R   A   G   C   I   V   C   N   T
 294 TTG ATA AAT GAA AAA TGG GGA CGG GAA GAG ATC ACC TAT GAC ACG CCT TTC AAA AGA GAA
      L   I   N   E   K   W   G   R   E   E   I   T   Y   D   T   P   F   K   R   E
 354 AAG TCT TTT GAG ATC GTG ATT ATG GTG CTG AAG GAC AAA TTC CAG GTG GCT GTA AAT GGA
      K   S   F   E   I   V   I   M   V   L   K   D   K   F   Q   V   A   V   N   G
 414 AAA CAT ACT CTG CTC TAT GGC CAC AGG ATC GGC CCA GAG AAA ATA GAC ACT CTG GGC ATT
      K   H   T   L   L   Y   G   H   R   I   G   P   E   K   I   D   T   L   G   I
 474 TAT GGC AAA GTG AAT ATT CAC TCA ATT GGT TTT AGC TTC AGC TCG GAC TTA CAA AGT ACC
      Y   G   K   V   N   I   H   S   I   G   F   S   F   S   S   D   L   Q   S   T
 534 CAA GCA TCT AGT CTG GAA CTG ACA GAG ATA GTT AGA GAA AAT GTT CCA AAG TCT GGC ACG
      Q   A   S   S   L   E   L   T   E   I   V   R   E   N   V   P   K   S   G   T
 594 CCC CAG CTT AGC CTG CCA TTC GCT GCA AGG TTG AAC ACC CCC ATG GGC CCT GGA CGA ACT
      P   Q   L   S   L   P   F   A   A   R   L   N   T   P   M   G   P   G   R   T
 654 GTC GTC GTT CAA GGA GAA GTG AAT GCA AAT GCC AAA AGC TTT AAT GTT GAC CTA CTA GCA
      V   V   V   Q   G   E   V   N   A   N   A   K   S   F   N   V   D   L   L   A
 714 GGA AAA TCA AAG GAT ATT GCT CTA CAC TTG AAC CCA CGC CTG AAT ATT AAA GCA TTT GTA
      G   K   S   K   D   I   A   L   H   L   N   P   R   L   N   I   K   A   F   V
 774 AGA AAT TCT TTT CTT CAG GAG TCC TGG GGA GAA GAA GAG AGA AAT ATT ACC TCT TTC CCA
      R   N   S   F   L   Q   E   S   W   G   E   E   E   R   N   I   T   S   F   P
 834 TTT AGT CCT GGG ATG TAC TTT GAG ATG ATA ATT TAT TGT GAT GTT AGA GAA TTC AAG GTT
      F   S   P   G   M   Y   F   E   M   I   I   Y   C   D   V   R   E   F   K   V
 894 GCA GTA AAT GGC GTA CAC AGC CTG GAG TAC AAA CAC AGA TTT AAA GAG CTC AGC AGT ATT
      A   V   N   G   V   H   S   L   E   Y   K   H   R   F   K   E   L   S   S   I
 954 GAC ACG CTG GAA ATT AAT GGA GAC ATC CAC TTA CTG GAA GTA AGG AGC TGG TAG
      D   T   L   E   I   N   G   D   I   H   L   L   E   V   R   S   W   *
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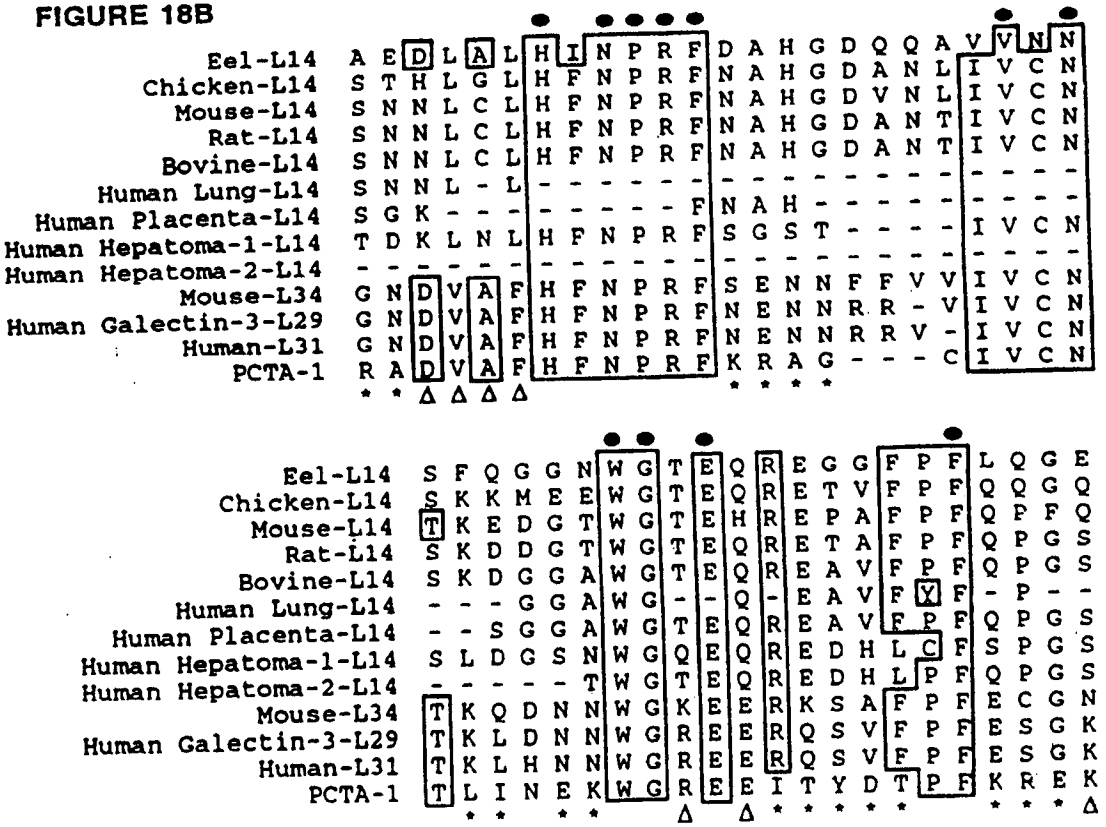
FIGURE 18B


Eel-L14 A E D L A L H I N P R F D A H G D Q Q A V V N N
Chicken-L14 S T H L G L H F N P R F N A H G D A N L I V C N
Mouse-L14 S N N L C L H F N P R F N A H G D V N L I V C N
Rat-L14 S N N L C L H F N P R F N A H G D A N T I V C N
Bovine-L14 S N N L C L H F N P R F N A H G D A N T I V C N
Human Lung-L14 S N N L - L - - - - - - - - - - - - - - - -
Human Placenta-L14 S G K - - - - - - - - F N A H - - - - - - - - -
Human Hepatoma-1-L14 T D K L N L H F N P R F S G S T - - - - I V C N
Human Hepatoma-2-L14 -
Mouse-L34 G N D V A F H F N P R F S E N N F F V V I V C N
Human Galectin-3-L29 G N D V A F H F N P R F N E N N R R - V I V C N
Human-L31 G N D V A F H F N P R F N E N N R R V - I V C N
PCTA-1 R A D V A F H F N P R F K R A G - - - C I V C N
* * Δ Δ Δ Δ * * * *
Eel-L14 S F Q G G N W G T E Q R E G G F P F L Q G E
Chicken-L14 S K K M E E W G T E Q R E T V F P F Q Q G Q
Mouse-L14 T K E D G T W G T E H R E P A F P F Q P F Q
Rat-L14 S K D D G T W G T E Q R E T A F P F Q P G S
Bovine-L14 S K D G G A W G T E Q R E A V F P F Q P G S
Human Lung-L14 - - - G G A W G T - E Q R - E A V F Y F - P - -
Human Placenta-L14 - - S G G A W G T - E Q R - R E A V F P F Q P G S
Human Hepatoma-1-L14 S L D G S N W G T Q E Q R R E D H L C F S P G S
Human Hepatoma-2-L14 - - - - - T W G T E Q R R E D H L P F Q P G S
Mouse-L34 T K Q D N N W G T K E E R K Q S A F P F E C G N
Human Galectin-3-L29 T K L D N N W G R R E E R Q S V F P F E S G K
Human-L31 T K L H N N W G R R E E R Q S V F P F E S G K
PCTA-1 T L I N E K W G R E E E I T Y D T P F K R E K
* * * * Δ Δ * * * * * * * * Δ

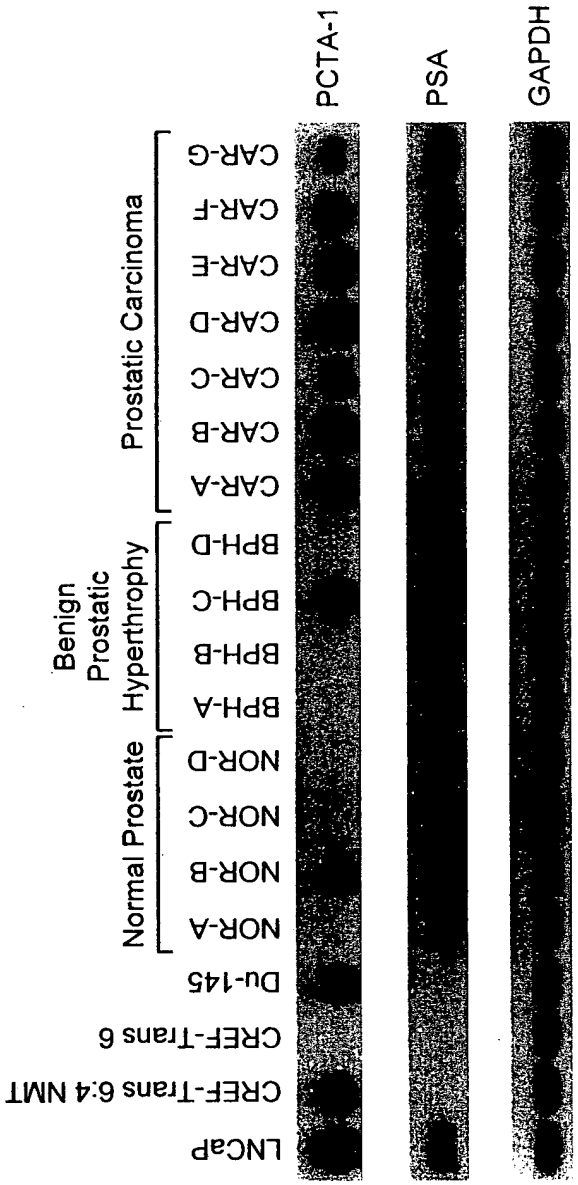


FIG. 19